

10/511561

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SEQUENCE LISTING

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Chen, Ping-Chi B
Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites and Antibodies Thereto

<130> IB-1807 PCT

<140> US 60/375,094

<141> 2003-04-21

<150> US 60/375,094

<151> 2002-04-22

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<170> PatentIn version 3.1

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Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu
65 70 75 80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met
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Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr
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Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu
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Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met
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Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu
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Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu
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Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn
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Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met
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Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu
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Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu
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Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile
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Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu
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Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp
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Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr
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Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu
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Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn
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Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val
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Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu
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Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met
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Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
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Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
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Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
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Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
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Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
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Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
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Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
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Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
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Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
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Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
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Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
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Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile
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Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu
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Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile
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Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro
675 680 685

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690 695 700

Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln
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Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu
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Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu
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Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val
755 760 765

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Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu
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820 825 830

His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu
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Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
850 855 860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
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Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
885 890 895

Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
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Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val

915

920

925

Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
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Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
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Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
980 985 990

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995 1000 1005

Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser
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Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Glu Lys Ser Pro
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His Pro Asn Ala Phe Lys Arg Leu Gly Ala Ser Leu Ala Phe Asn
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Phe Val Phe Glu Ala Leu Val Ile Tyr Met Glu Ser Leu Ala Leu
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Asp Ala Ile Asp His Leu Cys Arg Ile Ile Glu Lys Lys His Val
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Ser Leu Asn Lys Ala Lys Lys Arg Arg Leu Pro Arg Gly Phe Pro
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Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu
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Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile
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Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser
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Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser
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Phe Leu Ile Asn Thr Phe Glu Gly Gly Gly Cys Gly Gln Pro Ser
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Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe
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Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala
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Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala
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Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala
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Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala
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Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser
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Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val
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Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro
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Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu
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Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly
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Cys Val Asn Leu Met Lys Ala Leu Lys Met Ser Pro Tyr Lys Asp
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Ile Leu Glu Thr His Leu Arg Glu Lys Ile Thr Ala Gln Ser Ile
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Glu Glu Leu Cys Ala Val Asn Leu Tyr Gly Pro Asp Ala Gln Val
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Asp Arg Ser Arg Leu Ala Ala Val Val Ser Ala Cys Lys Gln Leu
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His Arg Ala Gly Leu Leu His Asn Ile Leu Pro Ser Gln Ser Thr
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Asp Leu His His Ser Val Gly Thr Glu Leu Leu Ser Leu Val Tyr
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Ser Glu Thr Ile Asn Thr Glu Leu Leu Lys Asn Leu Asp Leu Ala
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Gln Ile Asp Ser Ser Val Ser Phe Asn Thr Ser His Gly Ser Phe
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Pro Glu Val Phe Thr Thr Tyr Ile Ser Leu Leu Ala Asp Thr Lys
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Leu Asp Leu His Leu Lys Gly Gln Ala Val Thr Leu Leu Pro Phe
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Lys Lys Phe Leu Asp Ala Leu Glu Leu Ser Gln Ser Pro Met Leu
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Leu Glu Leu Met Thr Glu Val Leu Cys Arg Glu Gln Gln His Val
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Met Glu Glu Leu Phe Gln Ser Ser Phe Arg Arg Ile Ala Arg Arg
1775 1780 1785

Gly Ser Cys Val Thr Gln Val Gly Leu Leu Glu Ser Val Tyr Glu
1790 1795 1800

Met Phe Arg Lys Asp Asp Pro Arg Leu Ser Phe Thr Arg Gln Ser
1805 1810 1815

Phe Val Asp Arg Ser Leu Leu Thr Leu Leu Trp His Cys Ser Leu
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Asp Ala Leu Arg Glu Phe Phe Ser Thr Ile Val Val Asp Ala Ile

1835

1840

1845

Asp Val Leu Lys Ser Arg Phe Thr Lys Leu Asn Glu Ser Thr Phe
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Asp Thr Gln Ile Thr Lys Lys Met Gly Tyr Tyr Lys Ile Leu Asp
1865 1870 1875

Val Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu
1880 1885 1890

Ser Lys Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly
1895 1900 1905

Asn Glu Leu Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe
1910 1915 1920

Thr Glu Asn Met Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg
1925 1930 1935

Leu Tyr His Cys Ala Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys
1940 1945 1950

Cys Val Phe Asn Glu Leu Lys Phe Tyr Gln Gly Phe Leu Phe Ser
1955 1960 1965

Glu Lys Pro Glu Lys Asn Leu Leu Ile Phe Glu Asn Leu Ile Asp
1970 1975 1980

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1985 1990 1995

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2000 2005 2010

Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser Tyr Met Ser Ser Leu
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Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln Arg Asp
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Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
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Gln Val Pro Leu Lys Arg Leu Leu Asn Thr Trp Thr Asn Arg Tyr
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Val Ser Trp Val Gln Ser Tyr Cys Arg Leu Ser His Cys Arg Ser
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Ser Asn Asp Val Arg Ala Glu Leu Ala Lys Thr Pro Val Asn Lys
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Asp Pro Lys Ala Pro Gly Leu Gly Ala Phe Arg Arg Lys Phe Ile
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Asn Met Leu Leu Leu Lys Met Asn Lys Asp Ser Lys Pro Pro Gly

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3670

3675

Asn Leu Lys Glu Cys Ser Pro Trp Met Ser Asp Phe Lys Val Glu
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Gly Lys Pro Leu Pro Glu Tyr His Val Arg Ile Ala Gly Phe Asp
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Glu Arg Val Thr Val Met Ala Ser Leu Arg Arg Pro Lys Arg Ile
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Ile Ile Arg Gly His Asp Glu Arg Glu His Pro Phe Leu Val Lys
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Gly Gly Glu Asp Leu Arg Gln Asp Gln Arg Val Glu Gln Leu Phe
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Gln Val Met Asn Gly Ile Leu Ala Gln Asp Ser Ala Cys Ser Gln
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Arg Ala Leu Gln Leu Arg Thr Tyr Ser Val Val Pro Met Thr Ser
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Arg Leu Gly Leu Ile Glu Trp Leu Glu Asn Thr Val Thr Leu Lys
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Leu Ser Asp Pro Arg Ala Pro Pro Cys Glu Tyr Lys Asp Trp Leu
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Tyr Lys Gly Ala Asn Arg Thr Glu Thr Val Thr Ser Phe Arg Lys
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Ala Thr Gln Phe Leu Pro Val Pro Glu Leu Met Pro Phe Arg Leu
3950 3955 3960

Thr Arg Gln Phe Ile Asn Leu Met Leu Pro Met Lys Glu Thr Gly
3965 3970 3975

Leu Met Tyr Ser Ile Met Val His Ala Leu Arg Ala Phe Arg Ser
3980 3985 3990

Asp Pro Gly Leu Leu Thr Asn Thr Met Asp Val Phe Val Lys Glu
3995 4000 4005

Pro Ser Phe Asp Trp Lys Asn Phe Glu Gln Lys Met Leu Lys Lys
4010 4015 4020

Gly Gly Ser Trp Ile Gln Glu Ile Asn Val Ala Glu Lys Asn Trp
4025 4030 4035

Tyr Pro Arg Gln Lys Ile Cys Tyr Ala Lys Arg Lys Leu Ala Gly
4040 4045 4050

Ala Asn Pro Ala Val Ile Thr Cys Asp Glu Leu Leu Leu Gly His
4055 4060 4065

Glu Lys Ala Pro Ala Phe Arg Asp Tyr Val Ala Val Ala Arg Gly
4070 4075 4080

Ser Lys Asp His Asn Ile Arg Ala Gln Glu Pro Glu Ser Gly Leu
4085 4090 4095

Ser Glu Glu Thr Gln Val Lys Cys Leu Met Asp Gln Ala Thr Asp
4100 4105 4110

Pro Asn Ile Leu Gly Arg Thr Trp Glu Gly Trp Glu Pro Trp Met
4115 4120 4125

<210> 4
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (11)..(11)
<223> PHOSPHORYLATION at T2609

<400> 4

Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly
1 5 10 15

Thr Leu Gln Thr Arg
20

<210> 5
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (13)..(13)
<223> PHOSPHORYLATION at S2056

<400> 5

Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro
1 5 10 15

Arg Pro Ala Thr Gly Arg Phe Arg Arg Glu Gln Arg
20 25

<210> 6
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE

<222> (1)..(303)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (177)..(177)
<223> PHOSPHORYLATION at S2056

<400> 6

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile
290 295 300

<210> 7

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(388)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<400> 7

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
290 295 300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305 310 315 320

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
370 375 380

Asp Pro Asn Ser
385

<210> 8

<211> 821

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(821)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<220>

<221> MOD_RES

<222> (730)..(730)

<223> PHOSPHORYLATION at T2609

<400> 8

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu

65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
290 295 300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305 310 315 320

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
370 375 380

Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile
385 390 395 400

Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln
405 410 415

Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser Phe Val Arg
420 425 430

Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val Leu Gly Leu Ile Leu
435 440 445

Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Ser Leu Cys Glu
450 455 460

Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met Glu Asp Lys
465 470 475 480

Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro Leu Ala
485 490 495

Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys Phe His Gly
500 505 510

Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg Val Glu Gly
515 520 525

Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe Val Gln Val
530 535 540

Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu Asp Ile Ile
545 550 555 560

Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg Glu Leu Leu
565 570 575

Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr Cys Arg Glu
580 585 590

Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr Arg Asp Pro
595 600 605

Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys
610 615 620

Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu
625 630 635 640

Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr
645 650 655

Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu
660 665 670

Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser
675 680 685

Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
690 695 700

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser
705 710 715 720

Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr
725 730 735

Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val
740 745 750

Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr
755 760 765

Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser
770 775 780

Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu
785 790 795 800

Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser
805 810 815

Val Gly Pro Asp Phe
820

<210> 9

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(440)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (349)..(349)

<223> PHOSPHORYLATION at T2609

<400> 9

Ser Gly Lys Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu
1 5 10 15

Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys
20 25 30

Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser
35 40 45

Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly
50 55 60

Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser
65 70 75 80

Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met
85 90 95

Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro
100 105 110

Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
115 120 125

Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg
130 135 140

Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe
145 150 155 160

Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu
165 170 175

Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg
180 185 190

Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr
195 200 205

Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr
210 215 220

Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys
225 230 235 240

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
245 250 255

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
260 265 270

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
275 280 285

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
290 295 300

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
305 310 315 320

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
325 330 335

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
340 345 350

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
355 360 365

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
370 375 380

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
385 390 395 400

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
405 410 415

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
420 425 430

Leu Lys Ser Val Gly Pro Asp Phe
435 440

<210> 10
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(200)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (109)..(109)
<223> PHOSPHORYLATION at T2609

<400> 10

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
1 5 10 15

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
20 25 30

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
35 40 45

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
50 55 60

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
65 70 75 80

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
85 90 95

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
100 105 110

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
115 120 125

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
130 135 140

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
145 150 155 160

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
165 170 175

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
180 185 190

Leu Lys Ser Val Gly Pro Asp Phe
195 200

<210> 11

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(428)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (335)..(335)

<223> PHOSPHORYLATION at T2609

<400> 11

Gln Leu Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro
1 5 10 15

Gln Cys Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn
20 25 30

Met Ser Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val
35 40 45

Leu Gly Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu
50 55 60

Glu Ser Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn
65 70 75 80

Thr Met Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser
85 90 95

Phe Pro Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu
100 105 110

Pro Lys Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu
115 120 125

Cys Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys
130 135 140

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val
145 150 155 160

Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu
165 170 175

Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser
180 185 190

Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp
195 200 205

Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile
210 215 220

Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn
225 230 235 240

Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg
245 250 255

Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr
260 265 270

Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu
275 280 285

Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu
290 295 300

His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp
305 310 315 320

Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln
325 330 335

Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser
340 345 350

Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His
355 360 365

Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
370 375 380

Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser
385 390 395 400

Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg
405 410 415

Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys
420 425

<210> 12

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(273)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (180)..(180)

<223> PHOSPHORYLATION at T2609

<400> 12

Glu Arg Gln Lys Val Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys
1 5 10 15

Leu Lys Pro Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe
20 25 30

Val Ser His Pro Ser Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu
35 40 45

Met Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
50 55 60

Asp	Ser	Gln	Glu	Ile	Phe	Lys	Leu	Ala	Lys	Asp	Val	Leu	Ile	Gln	Gly
65					70				75				80		
Leu	Ile	Asp	Glu	Asn	Pro	Gly	Leu	Gln	Leu	Ile	Ile	Arg	Asn	Phe	Trp
					85				90				95		
Ser	His	Glu	Thr	Arg	Leu	Pro	Ser	Asn	Thr	Leu	Asp	Arg	Leu	Leu	Ala
							100		105				110		
Leu	Asn	Ser	Leu	Tyr	Ser	Pro	Lys	Ile	Glu	Val	His	Phe	Leu	Ser	Leu
							115		120				125		
Ala	Thr	Asn	Phe	Leu	Leu	Glu	Met	Thr	Ser	Met	Ser	Pro	Asp	Tyr	Pro
							130		135			140			
Asn	Pro	Met	Phe	Glu	His	Pro	Leu	Ser	Glu	Cys	Glu	Phe	Gln	Glu	Tyr
							145		150			155		160	
Thr	Ile	Asp	Ser	Asp	Trp	Arg	Phe	Arg	Ser	Thr	Val	Leu	Thr	Pro	Met
							165			170			175		
Phe	Val	Glu	Thr	Gln	Ala	Ser	Gln	Gly	Thr	Leu	Gln	Thr	Arg	Thr	Gln
							180		185			190			
Glu	Gly	Ser	Leu	Ser	Ala	Arg	Trp	Pro	Val	Ala	Gly	Gln	Ile	Arg	Ala
							195		200			205			
Thr	Gln	Gln	Gln	His	Asp	Phe	Thr	Leu	Thr	Gln	Thr	Ala	Asp	Gly	Arg
							210		215			220			
Ser	Ser	Phe	Asp	Trp	Leu	Thr	Gly	Ser	Ser	Thr	Asp	Pro	Leu	Val	Asp
							225		230			235		240	
His	Thr	Ser	Pro	Ser	Ser	Asp	Ser	Leu	Leu	Phe	Ala	His	Lys	Arg	Ser
							245		250			255			
Glu	Arg	Leu	Gln	Arg	Ala	Pro	Leu	Lys	Ser	Val	Gly	Pro	Asp	Phe	Gly
							260		265			270			
Lys
<210>	13														
<211>	140														

<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(140)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (49)..(49)
<223> PHOSPHORYLATION at T2609

<400> 13

Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met
1 5 10 15

Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp
20 25 30

Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu
35 40 45

Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser
50 55 60

Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln
65 70 75 80

Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe
85 90 95

Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser
100 105 110

Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu
115 120 125

Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe
130 135 140

<210> 14

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(102)
<223> HUMAN GENETIC ORIGIN

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> PHOSPHORYLATION at T2609

<400> 14

Val	Leu	Thr	Pro	Met	Phe	Val	Glu	Thr	Gln	Ala	Ser	Gln	Gly	Thr	Leu
1				5				10						15	

Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala
 20 25 30

Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln
 35 40 45

Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr
 50 55 60

Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe
 65 70 75 80

Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val
 85 90 95

Gly Pro Asp Phe Gly Lys
 100

<210> 15

<211> 13509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (6233)..(6235)
 <223> Encodes S2056

<220>
 <221> misc_feature
 <222> (7882)..(7884)
 <223> Encodes T2609

<400> 15

ggggcatttc	cgggtccggg	ccgagcgggc	gcacgcgcgg	gagcgggact	cggcggcatg	60
gcgggctccg	gagccggtgt	gcgttgctcc	ctgctgcggc	tgcaggagac	cttgtccgct	120
gcggaccgct	gcggtgctgc	cctggccggt	catcaactga	tccgcggcct	ggggcagggaa	180
tgcgtcctga	gcagcagccc	cgcggtgctg	gcattacaga	catcttttagt	ttttccaga	240

gatttcgggtt tgcttgttatt tgcgtccggaaat tcactcaaca gtattgaatt tcgtgaatgt	300
agagaagaaa tcctaaagtt tttatgttatt ttcttagaaaa aaatgggcca gaagatcgca	360
ccttactctg ttgaaattaa gaacacttgtt accagtgtt atacaaaaga tagagctgct	420
aatgtaaaa ttccagccct ggaccttctt attaagttac ttcatcacttt tagaagttct	480
agactcatgg atgaatttaa aattggagaa ttathtagta aattctatgg agaacttgca	540
ttgaaaaaaaaa aaataccaga tacagttta gaaaaagttat atgagctcctt aggattattt	600
ggtaagttc atcctagtga gatgataat aatgcagaaa acctgttccg cgctttctg	660
ggtaactta agaccagat gacatcagca gtaagagagc ccaaactacc tggcttggca	720
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<221> CDS
<222> (1)..(87)
<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature
<222> (37)..(37)

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<223> encodes S2056 residue

<400> 17

gatttctcaa ccggagttca gagctattca tacagctccc aagaccctag acctgccact      60
ggtcgtttc ggagacggga gcagcgg                                87

<210> 18

<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding the 1879-2182 peptide

<220>
<221> CDS
<222> (1)..(909)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (529)..(529)
<223> encodes S2056 residue

<400> 18

atgtattctc gccttccaa agatgatgtt catgctaagg aataaaaat taatcaagtt      60
ttccatggct cgtgtattac agaaggaaat gaacttacaa agacattgat taaattgtgc      120
tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt      180
taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtt      240
aaattttacc aaggtttct gttagtgaa aaaccagaaa agaacttgct tattttgaa      300
aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa      360
agaaagaaaa agtacattga aatttagaaa gaagccagag aagcagcaaa tggggattca      420
gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa      480
atagatcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct      540
agacctgcca ctggtcgtt tcggagacgg gagcagcggg accccacggt gcatgatgat      600
gtgctggagc tggagatgga cgagctaat cgccatgagt gcatggcgcc cctgacggcc      660
ctggtaagc acatgcacag aagcctggc ccgcctcaag gagaagagga ttcagtgcca      720
agagatcttc cttcttggat gaaattcctc catggcaaac tggaaatcc aatagtagcca      780
ttaaatatcc gtctttctt agccaagctt gttattaata cagaagaggt cttdcgccct      840
tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga      900
gaaggaatt                                909

```

<210> 19
 <211> 1164
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Cloned DNA sequence encoding the 1879-2267 peptide

 <220>
 <221> CDS
 <222> (1)..(1164)
 <223> HUMAN GENETIC ORIGIN

 <220>
 <221> misc_feature
 <222> (529)..(531)
 <223> encodes S2056 residue

 <400> 19

atgtattctc	gccttccaa	agatgatgtt	catgctaagg	aatcaaaaat	taatcaagtt	60
ttccatggct	cgtgtattac	agaaggaaat	gaacttacaa	agacattgat	taaattgtgc	120
tacgatgcat	ttacagagaa	catggcagga	gagaatcagc	tgctggagag	gagaagactt	180
taccattgtg	cagcatacaa	ctgcgccata	tctgtcatct	gctgtgtctt	caatgagtt	240
aaattttacc	aaggtttct	gtttagtgaa	aaaccagaaa	agaacttgct	tatTTTgaa	300
aatctgatcg	acctgaagcg	ccgctataat	tttcctgtag	aagttgaggt	tcctatggaa	360
agaaagaaaa	agtacattga	aatttaggaaa	gaagccagag	aagcagcaaa	tggggattca	420
gatggtcctt	cctatatgtc	ttccctgtca	tatttggcag	acagtaccct	gagtgaggaa	480
atagagtcaat	ttgatttctc	aaccggagtt	cagagctatt	catacagctc	ccaagaccct	540
agacctgcca	ctggtcgttt	tcggagacgg	gagcagcggg	accccacgg	gcatgatgat	600
gtgctggagc	tggagatgga	cgagctaat	cgccatgagt	gcatggcgcc	cctgacggcc	660
ctggtaagc	acatgcacag	aagcctggc	ccgcctcaag	gagaagagga	ttcagtgcca	720
agagatcttc	cttcttggat	gaaattcctc	catggcaaac	tggaaatcc	aatagtacca	780
ttaaatatcc	gtctttctt	agccaagctt	gttattaata	cagaagaggt	ctttcgccct	840
tacgcgaagc	actggcttag	cccccttgctg	cagctggctg	cttctgaaaa	caatggagga	900
gaaggaattc	actacatggt	ggttgagata	gtggccacta	ttctttcatg	gacaggctt	960
gccactccaa	caggggtccc	taaagatgaa	gtgttagcaa	atcgattgct	taatttccta	1020
atgaaacatg	tctttcatcc	aaaaagagct	gtgttagac	acaaccttga	aattataaag	1080
acccttgcg	agtgctggaa	ggattgttta	tccatccctt	ataggttaat	attgaaaaag	1140

tttccggta aagatcctaa ttct

1164

<210> 20

<211> 2463

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 1879-2700 peptide

<220>

<221> CDS

<222> (1)..(2463)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (529)..(531)

<223> encodes S2056 residue

<220>

<221> misc_feature

<222> (2188)..(2190)

<223> encodes T2609 residue

<400> 20

atgtattctc gccttccaa agatgatgtt catgctaagg aatcaaaaat taatcaagtt 60

ttccatggct cgtgtattac agaaggaaat gaacttacaa agacattgat taaattgtgc 120

tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt 180

taccatttgtc cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtt 240

aaattttacc aaggtttct gttagtgaa aaaccagaaa agaacttgct tattttgaa 300

aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa 360

agaaagaaaa agtacattga aatttagaaaa gaagccagag aagcagcaaa tggggattca 420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa 480

atagatcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct 540

agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggc gcatgatgat 600

gtgctggagc tggagatgga cgagctaat cgccatgagt gcatggcgcc cctgacggcc 660

ctggtaagc acatgcacag aagcctggc ccgcctcaag gagaagagga ttcagtgcca 720

agagatcttc cttcttggat gaaattcctc catggcaaac tggaaatcc aatagtagcca 780

ttaaatatcc gtctcttctt agccaagctt gttattaata cagaagaggt ct当地cgccct 840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga 900

gaaggaattc actacatggt gtttagata gtggccacta ttctttcatg gacaggctt 960

gccactccaa	caggggtccc	taaagatgaa	gtgttagcaa	atcgattgct	taatttccta	1020
atgaaaacatg	tctttcatcc	aaaaagagct	gtgttagac	acaacccctga	aattataaaag	1080
acccttgcg	agtgcgtgaa	ggattgtta	tccatccctt	ataggtaat	attgaaaag	1140
tttcccgta	aagatcctaa	ttctaaagac	aactcagtag	ggattcaatt	gctaggcatc	1200
gtgatggcca	atgacactgcc	tccctatgac	ccacagtgtg	gcatccagag	tagcgaatac	1260
ttccaggctt	tggtaataa	tatgtcctt	gtaagatata	aagaagtgt	tgccgctgca	1320
gcagaagttc	taggacttat	acttcgatat	gttatggaga	aaaaaaacat	actggaggag	1380
tctctgtgt	aactggttgc	gaaacaattg	aagcaacatc	agaatactat	ggaggacaag	1440
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aatgctgtgt	tctttctgct	gccaaaattt	catggagtgt	tgaaaacact	ctgtctggag	1560
gtggtaactt	gtcgtgtgga	ggaatgaca	gagctgtact	tccagttaaa	gagcaaggac	1620
ttcgttcaag	tcatgagaca	tagagatgt	gaaagacaaa	aagtatgtt	ggacataatt	1680
tataagatga	tgccaaagtt	aaaaccagta	gaactccgag	aacttctgaa	ccccgttgt	1740
gaattcgttt	cccatccttc	tacaacatgt	agggacaaa	tgtataatat	tctcatgtgg	1800
attcatgata	attacagaga	tccagaaagt	gagacagata	atgactccca	ggaaatattt	1860
aagttggcaa	aagatgtgct	gattcaagga	ttgatcgatg	agaaccctgg	acttcaatta	1920
attattcgaa	atttctggag	ccatgaaact	agttacctt	caaatacctt	ggaccggttt	1980
ctggcactaa	attccttata	ttctcctaag	atagaagtgc	acttttaag	tttagcaaca	2040
aattttctgc	tcgaaatgac	cagcatgagc	ccagattatc	caaaccctt	gttcgagcat	2100
cctctgtcag	aatgcgaatt	tcaagaaat	accattgatt	ctgattggcg	tttccgaagt	2160
actgttctca	ctccgatgtt	tgtggagacc	caggcctccc	agggcactct	ccagaccctgt	2220
acccaggaag	ggtccctctc	agctcgctgg	ccagtgccag	ggcagataag	ggccacccag	2280
cagcagcatg	acttcacact	gacacagact	gcagatggaa	gaagctcatt	tgattggctg	2340
accgggagca	gcactgaccc	gctggtcgac	cacaccagtc	cctcatctga	ctccttgctg	2400
tttggccaca	agaggagtga	aaggttacag	agagcacccct	tgaagtca	ggggcctgat	2460
ttt						2463

<210> 21

<211> 1320

<212> DNA

<213> Artificial sequence

<220>

<223> cDNA sequence encoding the 2261-2700 peptide

<220>

<221> CDS

<222> (1)..(1320)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (1045)..(1047)

<223> encodes T2609 residue

<400> 21

tccggtaaag atcctaattc taaagacaac tcagtaggga ttcaattgct aggcatcgta	60
atggccaatg acctgcctcc ctatgaccga cagtgtggca tccagagtag cgaataacttc	120
caggctttgg tgaataatat gtccttgta agatataaag aagtgtatgc cgctgcagca	180
gaagttctag gacttatact tcgatatgtt atggagagaa aaaacatact ggaggagtct	240
ctgtgtgaac tggttgcgaa acaattgaag caacatcaga atactatgga ggacaagttt	300
attgtgtgct tgaacaaagt gaccaagagc ttccctcctc ttgcagacag gttcatgaat	360
gctgtgttct ttctgctgcc aaaatttcat ggagtgttga aaacactctg tctggagggtg	420
gtactttgtc gtgtggaggg aatgacagag ctgtacttcc agttaaagag caaggacttc	480
gttcaagtca tgagacatag agatgatgaa agacaaaaag tatgtttgga cataatttat	540
aagatgatgc caaagttaaa accagtagaa ctccgagaac ttctgaaccc cggtgtggaa	600
ttcgtttccc atccttctac aacatgttagg gaacaaatgt ataatattct catgtggatt	660
catgataatt acagagatcc agaaagttag acagataatg actcccagga aatatttaag	720
ttggcaaaag atgtgctgat tcaaggattt atcgatgaga accctggact tcaattaatt	780
attcgaattt tctggagcca taaaacttagg ttaccttcaa ataccttggc ccgttgcgt	840
gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagttt agcaacaaat	900
tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct	960
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcggtt ccgaagtact	1020
gttctcaactc cgatgtttgt ggagacccag gcctcccagg gcactctcca gaccgtacc	1080
caggaagggt ccctctcagc tcgctggcca gtggcaggc agataagggc cacccagcag	1140
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc	1200
gggagcagca ctgacccgct ggtcgaccac accagtcct catctgactc cttgctgttt	1260
gcccacacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt	1320

<210> 22

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<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding the 2500-2700 peptide

<220>
<221> CDS
<222> (1)..(600)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (325)..(327)
<223> encodes T2609 residue

<400> 22

ttggcaaaag atgtgctgat tcaaggattt atcgatgaga accctggact tcaattaatt      60
attcgaaatt tctggagcca tgaaaacttagg ttaccttcaa ataccttggc ccggttgctg      120
gcactaaatt ccttatattt tcctaagata gaagtgcact ttttaagttt agcaacaaat      180
tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct      240
ctgtcagaat gcgaatttca ggaatataacc attgattctg attggcgttt ccgaagtact      300
gttctcaactc cgatgttgtt ggagacccag gcctcccagg gcactctcca gaccctgtacc      360
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataaggc cacccagcag      420
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc      480
gggagcagca ctgaccgct ggtcgaccac accagtccct catctgactc cttgctgttt      540
gcccacacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgattt      600

<210> 23

<211> 1284
<212> DNA
<213> Artificial sequence

<220>
<223> cDNA sequence encoding 2275-2702 peptide

<220>
<221> CDS
<222> (1)..(1284)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (1003)..(1005)
<223> encodes T2609 residue

<400> 23

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caattgctag	gcatcgtag	ggccaatgac	ctgcctccct	atgaccacaca	gtgtggcatc	60
cagagtagcg	aataacttcca	ggctttggtg	aataatatgt	cctttgttaag	atataaagaa	120
gtgtatgccg	ctgcagcaga	agttcttagga	cttatacttc	gatatgttat	ggagagaaaa	180
aacatactgg	aggagtctct	gtgtgaactg	gttgcgaaac	aattgaagca	acatcagaat	240
actatggagg	acaagtttat	tgtgtgcttg	aacaaagtga	ccaagagctt	ccctcctctt	300
gcagacaggt	tcatgaatgc	tgtgttcttt	ctgctgccaa	aatttcatgg	agtgttgaaa	360
acactctgtc	tggaggtgg	actttgtcgt	gtggagggaa	tgacagagct	gtacttccag	420
ttaaagagca	aggacttcgt	tcaagtcatg	agacatagag	atgatgaaag	acaaaaagta	480
tgtttggaca	taatttataa	gatgatgcca	aagtaaaac	cagtagaact	ccgagaactt	540
ctgaaccccg	ttgtggaatt	cgtttcccatt	ccttctacaa	catgtaggaa	acaaatgtat	600
aatattctca	tgtggattca	tgataattac	agagatccag	aaagtgagac	agataatgac	660
tcccagggaaa	tatttaagtt	ggcaaaagat	gtgctgattc	aaggattgat	cgatgagaac	720
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tggcgttcc	gaagtactgt	tctcactccg	atgtttgtgg	agacccaggc	ctcccaggc	1020
actctccaga	cccgtaacca	ggaagggtcc	ctctcagctc	gctggccagt	ggcagggcag	1080
ataagggccca	cccagcagca	gcatgacttc	acactgacac	agactgcaga	tggaagaagc	1140
tcatattgatt	ggctgaccgg	gagcagcact	gaccgcgtgg	tcgaccacac	cagtcctca	1200
tctgactcct	tgctgtttgc	ccacaagagg	agtgaaaggt	tacagagagc	acccttgaag	1260
tcagtggggc	ctgattttgg	gaaa				1284

<210> 24

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2429-2072 peptide

<220>

<221> CDS

<222> (1)..(819)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

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<222> (538)..(540)
<223> encodes T2609 residue

<400> 24

gaaagacaaa aagtatgtt ggacataatt tataagatga tgccaaagtt aaaaccagta      60
gaactccgag aacttctgaa ccccgttgc gaattcggtt cccatccttc tacaacatgt      120
aggaaacaaa tgtataatat tctcatgtgg attcatgata attacagaga tccagaaaagt      180
gagacagata atgactccca gaaaaatattt aagttggcaa aagatgtgct gattcaagga      240
ttgatcgatg agaacccctgg acttcaatta attattcgaa atttctggag ccatgaaaact      300
aggttacctt caaatacctt ggaccgggtt ctggcactaa attccttata ttctcctaag      360
atagaagtgc acttttaag ttagcaaca aattttctgc tcgaaatgac cagcatgagc      420
ccagattatc caaaccctt gttcgagcat cctctgtcag aatgcgaatt tcaggaatat      480
accattgatt ctgatggcg tttccgaagt actgttctca ctccgatgtt tgtggagacc      540
caggcctccc agggcactct ccagaccgt acccaggaag ggtccctctc agctcgctgg      600
ccagtggcag ggcagataag gcccacccag cagcagcatg acttcacact gacacagact      660
gcagatggaa gaagctcatt tgattggctg accgggagca gcactgaccc gctggtcgac      720
cacaccagtc cctcatctga ctccttgctg tttgccaca agaggagtga aaggttacag      780
agagcaccct tgaagtcagt ggggcctgat tttgggaaa                         819

<210> 25

<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA Sequence encoding 2561-2700 peptide

<220>
<221> CDS
<222> (1)..(420)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (145)..(147)
<223> Encodes T2609 residue

<400> 25

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct      60
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcggtt ccgaagtact      120
gttctcactc cgatgttgtt ggagacccag gcctcccagg gcactctcca gaccctgatc      180

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caggaagggt ccctctcagc tcgctggcca gtggcagggc agataaggc cacccagcag	240
cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc	300
gggagcagca ctgaccgct ggtcgaccac accagtccct catctgactc cttgctgttt	360
gcccacacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt	420
<210> 26	
<211> 306	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> cDNA sequence encoding 2600-2702 peptide	
<220>	
<221> CDS	
<222> (1)..(306)	
<223> HUMAN GENETIC ORIGIN	
<220>	
<221> misc_feature	
<222> (25)..(27)	
<223> Encodes T2609 residue	
<400> 26	
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cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc	180
gggagcagca ctgaccgct ggtcgaccac accagtccct catctgactc cttgctgttt	240
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gggaaa	306
<210> 27	
<211> 34	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Primer to create T2609A mutation	
<400> 27	
tccgatgttt gtggaggacc aggccctccca gggc	34
<210> 28	
<211> 34	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Reverse primer to create T2609A mutation

<400> 28

gcctggag gcctggcct ccacaaacat cgga

34